



ST00004 US DIV Sequence Listing.txt
SEQUENCE LISTING

<110> Maury, Isabella
Mercken, Luc
Fournier, Alain

<120> Partners of the PTB1 Domain of FE65, Preparation and Uses

<130> ST00004-US

<140> 09/780,996

<141> 2001-02-09

<150> FR00/01628

<151> 2000-02-10

<150> US 60/198,500

<151> 2000-04-18

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1

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cgtcagctct cttaccacaa aaacaacctg catgacccca tgtctggggg ctgggggggaa     180
ggaaaggatc tgctactgca gctggaggat gagacactaa agctagtgga gccacagagc     240
caggcactgc tgcacgccc aacctatcgc agcatccgcg tgtggggcgt cgggcggggac     300
agtggaaggg actttgccta cgtagctcgt gataagctga cccagatgct caagtgccac     360
gtgtttcgtc gtgaggcacc tgccaagaac atcgccacca gcctgcatga gatctgctct     420
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<210> 2

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2

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Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys Cys Phe Ala Val Arg Ser
1              5              10              15
```

```
Leu Gly Trp Val Glu Met Thr Glu Glu Glu Leu Ala Pro Gly Arg Ser
20              25              30
```

ST00004 US DIV Sequence Listing.txt

Ser Val Ala Val Asn Asn Cys Ile Arg Gln Leu Ser Tyr His Lys Asn
35 40 45

Asn Leu His Asp Pro Met Ser Gly Gly Trp Gly Glu Gly Lys Asp Leu
50 55 60

Leu Leu Gln Leu Glu Asp Glu Thr Leu Lys Leu Val Glu Pro Gln Ser
65 70 75 80

Gln Ala Leu Leu His Ala Gln Pro Ile Ile Ser Ile Arg Val Trp Gly
85 90 95

Val Gly Arg Asp Ser Gly Arg Asp Phe Ala Tyr Val Ala Arg Asp Lys
100 105 110

Leu Thr Gln Met Leu Lys Cys His Val Phe Arg Cys Glu Ala Pro Ala
115 120 125

Lys Asn Ile Ala Thr Ser Leu His Glu Ile Cys Ser Lys Ile Met Ala
130 135 140

Glu Arg Arg Asn Ala
145

<210> 3
<211> 28
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 3
cttcccgggt cccccacgga ataccaac

28

<210> 4
<211> 27
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 4
ggggtcgacg gcattacgcc gttcggc

27

<210> 5

ST00004 US DIV Sequence Listing.txt

<211> 18
<212> DNA
<213> Artificial

<220>
<223> GAL4TA oligonucleotide

<400> 5
ccactacaat ggatgatg 18

<210> 6
<211> 1047
<212> DNA
<213> Homo sapiens

<400> 6
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caccagctt ttgtcaacta ctctaccagc cagaagatct cccgccctgg ggactcggat 120
gactcccga gcgatgaacag tgtgtctctc ttaccatcc tgaacccat ttattcgatc 180
accagggatg ttctttacac tatctgtaat ccttgtggcc ctgtccagag aattgtcatt 240
ttcaggaaga atggagttca ggcgatggtg gaatttgact cagttcaaag tgcccagcgg 300
gccaaggcct ctctcaatgg ggctgatatc tattctggct gttgactct gaagatcgaa 360
tacgcaaagc ctacacgctt gaatgtgttc aagaatgatc aggatacttg ggactacaca 420
aaccccaatc tcagtggaca aggtgaccct ggcagcaacc ccaacaaacg ccagaggcag 480
ccccctctcc tgggagatca cccgcgagaa tatggagggc cccacggtgg gtaccacagc 540
cattaccatg atgagggtca cgggcccccc ccacctcact acgaaggag aaggatgggt 600
ccaccagtgg ggggtcaccg tcggggccca agtcgctacg gccccagta tgggcacccc 660
ccaccccctc cccaccacc cgagtatggc cctcacgcg acagccctgt gctcatggtc 720
tatggcttgg atcaatctaa gatgaactgt gaccgagtct tcaatgtctt ctgcttatat 780
ggcaatgtgg agaagggtgaa attcatgaaa agcaagccgg gggccgcat ggtggagatg 840
gctgatggct acgctgtaga ccgggccatt acccacctca acaacaactt catgtttggg 900
cagaagctga atgtctgtgt ctccaagcag ccagccatca tgcttgggtca gtcatacggg 960
ttggaagacg ggtcttgcag ttacaaagac ttcagtgaat cccggaacaa tcggttctcc 1020
acccagagc aggcagccaa gaaccgc 1047

<210> 7
<211> 349
<212> PRT
<213> Homo sapiens

ST00004 US DIV Sequence Listing.txt

<400> 7

Val Leu Gly Ala Cys Asn Ala Val Asn Tyr Ala Ala Asp Asn Gln Ile
1 5 10 15

Tyr Ile Ala Gly His Pro Ala Phe Val Asn Tyr Ser Thr Ser Gln Lys
20 25 30

Ile Ser Arg Pro Gly Asp Ser Asp Asp Ser Arg Ser Val Asn Ser Val
35 40 45

Leu Leu Phe Thr Ile Leu Asn Pro Ile Tyr Ser Ile Thr Thr Asp Val
50 55 60

Leu Tyr Thr Ile Cys Asn Pro Cys Gly Pro Val Gln Arg Ile Val Ile
65 70 75 80

Phe Arg Lys Asn Gly Val Gln Ala Met Val Glu Phe Asp Ser Val Gln
85 90 95

Ser Ala Gln Arg Ala Lys Ala Ser Leu Asn Gly Ala Asp Ile Tyr Ser
100 105 110

Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Lys Pro Thr Arg Leu Asn
115 120 125

Val Phe Lys Asn Asp Gln Asp Thr Trp Asp Tyr Thr Asn Pro Asn Leu
130 135 140

Ser Gly Gln Gly Asp Pro Gly Ser Asn Pro Asn Lys Arg Gln Arg Gln
145 150 155 160

Pro Pro Leu Leu Gly Asp His Pro Ala Glu Tyr Gly Gly Pro His Gly
165 170 175

Gly Tyr His Ser His Tyr His Asp Glu Gly Tyr Gly Pro Pro Pro Pro
180 185 190

His Tyr Glu Gly Arg Arg Met Gly Pro Pro Val Gly Gly His Arg Arg
195 200 205

Gly Pro Ser Arg Tyr Gly Pro Gln Tyr Gly His Pro Pro Pro Pro Pro
210 215 220

Pro Pro Pro Glu Tyr Gly Pro His Ala Asp Ser Pro Val Leu Met Val

225 230 235 240

ST00004 US DIV Sequence Listing.txt

```

gggtggtctcc caattgtcgc aaagattctc aatactcggg atcccatagt taaggaaaag 420
gctttaattg tcctgaataa cttgagtgtg aatgctgaaa atcagcgcag gcttaaagta 480
tacatgaatc aagtgtgtga tgacacaatc acttctcgct tgaactcatc tgtgcagctt 540
gctggactga gattgcttac aaatatgact gttactaatg agtatcagca catgcttgct 600
aattccattt ctgacttttt tcgtttattt tcagcgggaa atgaagaaac caaacttcag 660
gttctgaaac tccttttgaa tttggctgaa aatccagcca tgactagggg actgctcagg 720
gcccaagtac catcttcact gggctccctc ttttaataaga aggagaacaa agaagttatt 780
cttaaacttc tggatcatatt tgagaacata aatgataatt tcaaattggg agaaaatgaa 840
cctactcaga atcaattcgg tgaaggttca ctttttttct ttttaaaaga atttcaagt 900
tgtgctgata aggntctggg aatagaaagt caccatgatt ttttggtgaa agtaaaagtt 960
ggaaaattca tggccaaact tgctgaacat atgttcccaa agagccagga ataacacctt 1020
gattttgtaatttagaagca acacacattg taaactattc attttctcca ccttgtttat 1080
atggtaaagg aatcctttca gctgccagtt ttgaataatg aatatcatat tgtatcatca 1140
atgctgatat ttaactgagt tggctcttag gtttaagatg gataaatgaa tatcactact 1200
tgttctgaaa acatgtttgt tgctttttat ctcgctgcct agattgaaat attttgctat 1260
ttcttctggc taaag 1275

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```

<210> 9
<211> 337
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> X=G, D, V, or A

<220>
<221> misc_feature
<222> (305)..(305)
<223> Xaa can be any naturally occurring amino acid

<400> 9

```

```

Arg Gly Asp Val Asp Asp Ala Gly Asp Cys Ser Gly Ala Arg Tyr Asn
1           5           10          15

```

```

Asp Trp Ser Asp Asp Asp Asp Ser Asn Glu Ser Lys Ser Ile Val
20           25          30

```

```

Trp Tyr Pro Pro Trp Ala Arg Ile Gly Thr Glu Ala Gly Thr Arg Ala

```

ST00004 US DIV Sequence Listing.txt

35

40

45

```

• Arg Ala Arg Ala Arg Ala Arg Ala Thr Arg Ala Arg Arg Ala Val Gln
  50                      55                      60

•
Lys Arg Ala Ser Pro Asn Ser Asp Asp Thr Val Leu Ser Pro Gln Glu
65                      70                      75                      80

Leu Gln Lys Val Leu Cys Leu Val Glu Met Ser Glu Lys Pro Tyr Ile
      85                      90                      95

Leu Glu Ala Ala Leu Ile Ala Leu Gly Asn Asn Ala Ala Tyr Ala Phe
      100                      105                      110

Asn Arg Asp Ile Ile Arg Asp Leu Gly Gly Leu Pro Ile Val Ala Lys
      115                      120                      125

Ile Leu Asn Thr Arg Asp Pro Ile Val Lys Glu Lys Ala Leu Ile Val
      130                      135                      140

Leu Asn Asn Leu Ser Val Asn Ala Glu Asn Gln Arg Arg Leu Lys Val
      145                      150                      155                      160

Tyr Met Asn Gln Val Cys Asp Asp Thr Ile Thr Ser Arg Leu Asn Ser
      165                      170                      175

Ser Val Gln Leu Ala Gly Leu Arg Leu Leu Thr Asn Met Thr Val Thr
      180                      185                      190

Asn Glu Tyr Gln His Met Leu Ala Asn Ser Ile Ser Asp Phe Phe Arg
      195                      200                      205

Leu Phe Ser Ala Gly Asn Glu Glu Thr Lys Leu Gln Val Leu Lys Leu
      210                      215                      220

Leu Leu Asn Leu Ala Glu Asn Pro Ala Met Thr Arg Glu Leu Leu Arg
      225                      230                      235                      240

Ala Gln Val Pro Ser Ser Leu Gly Ser Leu Phe Asn Lys Lys Glu Asn
      245                      250                      255

Lys Glu Val Ile Leu Lys Leu Leu Val Ile Phe Glu Asn Ile Asn Asp
      260                      265                      270

```

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Asn Phe Lys Trp Glu Glu Asn Glu Pro Thr Gln Asn Gln Phe Gly Glu
275 280 285

Gly Ser Leu Phe Phe Phe Leu Lys Glu Phe Gln Val Cys Ala Asp Lys
290 295 300

Xaa Leu Gly Ile Glu Ser His His Asp Phe Leu Val Lys Val Lys Val
305 310 315 320

Gly Lys Phe Met Ala Lys Leu Ala Glu His Met Phe Pro Lys Ser Gln
325 330 335

Glu

<210> 10
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Fragment of cytoplasmic domain of APP

<400> 10

Tyr Glu Asn Pro Thr Tyr
1 5

<210> 11
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fragment of SEQ ID NO:7

<400> 11

Asn Pro Ile Tyr
1